Amendments to the Specification:

Please amend the paragraph on page 11, line 35, through page 12, line 4, beginning, "For example, in the Examples, the homologies as shown in Table..." as follows:

--For example, in ~~the Examples~~ Example 2, the homologies as shown in Table 1 were calculated using Maximum Matching, of the genetic information processing software, GENETYX (~~Takashi~~ Takeishi K. and ~~Gotho~~ Gotoh O. ~~(1984)~~ (1982) J. Biochem. 92:1173-1177). The parameters in this method are as follows:

Matching condition: matches= -1, mismatches= 1, gaps= 1, *N+= 2--

Please amend the paragraph on page 13, lines 11-23, beginning, "The preferable partial amino acid sequences of the present..." as follows:

--The preferable partial amino acid sequences of the present invention may comprise, within the amino acid sequences encoded by the polynucleotides of a) to d), ~~nucleotide~~ amino acid sequences that are predicted to be epitopes. Those skilled in the art can predict epitopes based on test amino acid sequences. Epitopes are predicted according to various characteristics of the amino acid sequence. Information on hydrophilicity/hydrophobicity, electric charges, glycosylation sequences, disulfide bonds, protein secondary structures, T-cell antigenic sites, and such is used to predict the parameters. Protein secondary structure can be predicted by the Chou-Fasman method, Robson method, or such. Furthermore, T-cell antigenic sites are predicted based on IA patterns and Rothbard/Taylor patterns.--

Please amend the paragraph on page 17, lines 2-9, beginning, "A baculovirus (Autographa californica nuclear polyhedrosis..." as follows:

--A baculovirus (Autographa californica nuclear polyhedrosis virus; AcNPV), uses insects as a host and comprises a double-stranded circular DNA genome. Polyhedra containing many viral particles are produced in the nuclei of infected cells, and serve as the infection source. The expression of the polyhedral protein, ~~"polyhidrin"~~ "polyhedrin", which is one of the proteins constituting a polyhedron, is regulated by a powerful promoter. The baculovirus expression system utilizes the activity of this powerful ~~polyhidrin~~ polyhedrin promoter.--

Please amend the paragraph on page 17, lines 10-20, beginning, "The polyhidrin gene shows extremely high expression levels..." as follows:

--The ~~polyhidrin~~ polyhedrin gene shows extremely high expression levels in the later stage of infection. However, in cultured cells, it is not an essential protein for viral proliferation. Therefore, if the ~~polyhidrin~~ polyhedrin gene, which is downstream of the ~~polyhidrin~~ polyhedrin promoter, is substituted with an exogenous gene, high expression of the exogenous gene can be expected, as for ~~polyhidrin~~ polyhedrin. More specifically, the baculovirus expression system is constructed according to the following steps:

•subcloning exogenous genes into transfer vectors;

•preparing recombinant viruses; and

•expressing proteins.--

Please amend the paragraph on page 27, line 29, through page 28, line 1, beginning, "In addition, the present invention relates to methods of..." as follows:

--In addition, the present invention relates to methods of testing for feline infectious peritonitis virus infections, which comprise the steps of incubating cat serum with a protein comprising an amino acid sequence encoded by a

polynucleotide of any one of a) to e); and then detecting an antibody that binds to the protein. As indicated in ~~the Examples~~ Example 10, N proteins derived from KU-2 react strongly with the antisera of a wide range of FIPV strains. This supports the fact that the N proteins of KU-2 are highly useful as FIPV vaccines, and that they are also useful as diagnostic antigens.--

Please amend the paragraph on page 29, line 35, through page 30, line 5, beginning, "Fig. 2 shows the results of aligning the N-protein amino acid..." as follows:

--Fig. 2 shows the results of aligning the N-protein amino acid sequences of FIPV with closely related viruses. In order from the top, each sequence shows the amino acid sequence of the N protein of type I FIPV strain KU-2 (SEQ ID NO: 2), Black, UCD1, type II FIPV strain 79-1146, type II FECV strain 79-1683, CCV Insvc1, and TGEV ~~Purde~~ Purdue. In this figure, "..." indicates that the amino acid residue is the same as that of KU-2, and "-" indicates a gap.--

Please amend the paragraph on page 30, lines 6-10, beginning, "Fig. 3 shows a phylogenetic tree calculated from the amino..." as follows:

--Fig. 3 shows a phylogenetic tree calculated from the amino acid sequences of the N genes of type I FIPV strain KU-2, Black, UCD1, type II FIPV strain 79-1146, type II FECV strain 79-1683, CCV Insvc1, and TGEV ~~Purde~~ Purdue. The numbers in the figure indicate evolutionary distance.--

Please amend the paragraph on page 32, lines 25-31, beginning, "Fig. 18 is a photograph showing the results of a Western..." as follows:

--Fig. 18 is a photograph showing the results of a Western blotting assay to investigate the reactivity of the sera of feline coronavirus-infected cats against E. coli-expressed antigens. Each lane shows the result of reacting the serum of cats infected with the coronavirus strain indicated ~~at the top of the lanes~~ as "CAT

SERUM", using a filter blotted with the antigen indicated ~~immediately above the lane~~ as "EXPRESSED PROTEIN".--

Please amend the paragraph on page 36, lines 13-21, beginning, "Fig. 2 shows the amino acid sequence alignment of the N genes..." as follows:

--Fig. 2 shows the amino acid sequence alignment of the N genes derived from, respectively, the type I FIPV strains KU-2, Black, and UCD1, type II FIPV strain 79-1146, type II feline enteric coronavirus (FECV) strain 79-1683, canine coronavirus (CCV) strain Insvc1, and swine transmissible gastroenteritis virus (TGEV) strain ~~Purde~~ Purdue. Comparison of these amino acid sequences showed that the KU-2 strain gene comprises many characteristic amino acid mutations that are not present in the other six strains, that is, the KU-2 strain has an unique sequence.--

Please amend the paragraph on page 36, lines 22-27, beginning, "Table 1 shows the amino acid sequence homology and nucleotide..." as follows:

-- Table 1 shows the amino acid sequence homology and nucleotide sequence homology of the N proteins. The homologies in the table were calculated using Maximum Matching from the genetic information processing software, GENETYX. The parameters are shown above (~~Takashi~~ Takeishi K. and ~~Gotho~~ Gotoh O. ~~(1984)~~ (1982) J. Biochem. 92:1173-1177).--

Please amend Table 2 on page 44 as follows:

Table 2

Groups	Cat No.	Neutralizing antibody titer			
		With complement		Without complement	
		Antigen inoculation	70 days after inoculation	Antigen inoculation	70 days after inoculation
Baculovirus recombinant N protein-immunized group	217	<10	<10	<10	<10
	221	<10	<10	<10	<10
	191	<10	<10	<10	<10
	6	<10	<10	<10	<10
~~SF-9-immunized~~ SF-9 cell-derived antigen-immunized antigen group	163	<10	<10	<10	<10
	210	<10	<10	<10	<10
	170	<10	<10	<10	<10
	173	<10	<10	<10	<10

Please amend Table 6 on page 55 as follows:

Table 6

	Groups	Cat No.	Days after FIPV 79-1146 strain inoculation (days)					
			0	3	6	9	12	15
Virus isolation using fcwf-4	Baculovirus recombinant N protein-immunized group	177	-	-	-	-	+	+
		242	-	-	-	-	-	-
		245	-	-	-	-	-	-
		247	-	-	-	-	+	-
	Purified FIPV N protein-immunized group	175	-	-	-	-	-	-
		180	-	-	+	-	+	-
		243	-	-	-	-	-	-
		252	-	-	-	-	-	-
	SF-9 cell-derived antigen-immunized group	178	-	-	-	-	-	-
		181	-	-	-	-	-	-
		244	-	-	-	-	-	-
		249	-	-	-	-	-	-

Detection of FCoV gene using RT-nPCR	Baculovirus recombinant N protein-immunized group	177	-	-	-	-	+	+
		242	-	-	-	-	-	-
		245	-	-	-	+	+	-
		247	-	-	-	-	+	-
	Purified FIPV N protein-immunized group	175	-	-	-	+	-	-
		180	-	-	+	-	+	-
		243	-	-	-	-	-	-
		252	-	-	-	-	-	-
	SF-9 cell-derived antigen-immunized group	178	-	-	-	+	-	-
		181	-	-	-	-	-	+
		244	-	-	+	-	-	-
		249	-	-	-	-	-	-

+: Virus was isolated, or FCoV gene was detected
-: Virus was not isolated, ~~or~~ and FCoV gene was detected

Please amend Table 7 on page 56 as follows:

Table 7

	Groups	Cat No.	Days after FIPV 79-1146 strain inoculation (days)					
			0	3	6	9	12	15
Virus isolation using fcwf-4	Baculovirus recombinant N protein-immunized group	177	-	+	+	+	-	-
		242	-	+	+	-	-	-
		245	-	+	+	+	-	-
		247	-	+	+	+	-	-
	Purified FIPV N protein-immunized group	175	-	+	+	+	-	-
		180	-	-	+	-	-	-
		243	-	+	+	-	-	-
		252	-	+	+	+	-	-
	SF-9 cell-derived antigen-immunized group	178	-	+	+	-	-	-
		181	-	+	-	+	-	-
		244	-	+	-	+	-	-
		249	-	+	+	+	-	-
Detection of FCoV gene using RT-nPCR	Baculovirus recombinant N protein-immunized group	177	-	+	+	+	-	-
		242	-	+	+	-	-	-
		245	-	+	+	+	-	-
		247	-	+	+	+	-	-
	Purified FIPV N protein-immunized	175	-	+	+	+	-	-
		180	-	+	+	+	+	+

	group	243	-	+	+	-	-	-
		252	-	+	+	+	-	-
	SF-9 cell-derived antigen-immunized group	178	-	+	+	-	+	-
		181	-	+	-	+	-	-
		244	-	+	-	+	-	-
		249	-	+	+	+	+	-

+: Virus was isolated, or FCoV gene was detected
-: Virus was not isolated, ~~or~~ and FCoV gene was detected